

<110> Korea Research Institute of Bioscience and Biotechnology
 <120> Rapid screening method of translational fusion partners for
 producing recombinant proteins and translational fusion partners
 screened therefrom
 <150> KR10-2004-0003957
 <151> 2004-01-19
 <160> 45
 <170> KopatentIn 1.71
 <210> 1
 <211> 105
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <220>
 <221> PEPTIDE
 <222> (1)..(105)
 <223> TFP1

<400> 1
 Met Phe Asn Arg Phe Asn Lys Phe Gln Ala Ala Val Ala Leu Ala Leu
 1 5 10 15
 Leu Ser Arg Gly Ala Leu Gly Asp Ser Tyr Thr Asn Ser Thr Ser Ser
 20 25 30
 Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala
 35 40 45
 Thr Ala Ser Asp Ser Leu Ser Ser Ser Asp Gly Thr Val Tyr Leu Pro
 50 55 60
 Ser Thr Thr Ile Ser Gly Asp Leu Thr Val Thr Gly Lys Val Ile Ala
 65 70 75 80
 Thr Glu Ala Val Glu Val Ala Ala Gly Gly Lys Leu Thr Leu Leu Asp
 85 90 95
 Gly Glu Lys Tyr Val Phe Ser Ser Asp
 100 105

<210> 2
 <211> 430
 <212> DNA
 <213> *Saccharomyces cerevisiae*
 <220>
 <221> gene
 <222> (1)..(430)
 <223> TFP1

<400> 2
 gatcgtcata ttctactcttg ttctcataat agcagtcctaa gttttcatct ttgcaagctt 60
 tactatttct ttctttttat tggtaaactc tcgcccatta caaaaaaaaa agagatgttc 120
 aatcgtttta acaaattcca agctgctgtc gctttggccc tactctctcg cggcgctctc 180
 ggtgactctt acaccaatag cactctctcc gcagacttga gtctatcac ttccgtctcg 240
 tcagctagtg caagtgcac cgcttcgcac tcactttctt ccagtgacgg taccgtttat 300
 ttgccatcca caacaattag cggtgatctc acagttactg gtaaagtaat tgcaaccgag 360
 gccgtggaag tcgctgccgg tggtaagttg actttacttg acggtgaaaa atacgtcttc 420
 tcactgatac 430

<210> 3
 <211> 117

PCTA9411-6.txt

<212> PRT
 <213> Saccharomyces cerevisiae

<220>
 <221> PEPTIDE
 <222> (1)..(117)
 <223> TFP2

<400> 3
 Met Thr Pro Tyr Ala Val Ala Ile Thr Val Ala Leu Leu Ile Val Thr
 1 5 10 15
 Val Ser Ala Leu Gln Val Asn Asn Ser Cys Val Ala Phe Pro Pro Ser
 20 25 30
 Asn Leu Arg Gly Lys Asn Gly Asp Gly Thr Asn Glu Gln Tyr Ala Thr
 35 40 45
 Ala Leu Leu Ser Ile Pro Trp Asn Gly Pro Pro Glu Ser Leu Arg Asp
 50 55 60
 Ile Asn Leu Ile Glu Leu Glu Pro Gln Val Ala Leu Tyr Leu Leu Glu
 65 70 75 80
 Asn Tyr Ile Asn His Tyr Tyr Asn Thr Thr Arg Asp Asn Lys Cys Pro
 85 90 95
 Asn Asn His Tyr Leu Met Gly Gly Gln Leu Gly Ser Ser Ser Asp Asn
 100 105 110
 Arg Ser Leu Asn Asp
 115

<210> 4
 <211> 424
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>
 <221> gene
 <222> (1)..(424)
 <223> TFP2

<400> 4
 gatctcattg gattcaagag aaagaaactc tatactggcg ccaaattagc agtgtcaaatt 60
 ttcgaaaagg tgatgacgcc ctatgcagta gcaattaccg tggccttact aattgtaaca 120
 gtgagcgcac tccaggtcaa caattcatgt gtcgcttttc cgccatcaaa tctcagaggo 180
 aaaaatggag acggtactaa tgaacagtat gcaactgcac tactttctat tccctggaat 240
 ggacctcctg agtcattgag ggatattaat cttattgaac tcgaaccgca agttgcactc 300
 tatttgctcg aaaattatat taaccattac tacaacacca caagagacaa taagtgcctt 360
 aataaccact acctaatggg agggcagttg ggtagctcat cggataatag gagtttgaac 420
 gatc 424

<210> 5
 <211> 104
 <212> PRT
 <213> Saccharomyces cerevisiae

<220>
 <221> PEPTIDE
 <222> (1)..(104)
 <223> TFP3

<400> 5
 Met Gln Phe Lys Asn Val Ala Leu Ala Ala Ser Val Ala Ala Leu Ser
 1 5 10 15

PCTA9411-6.txt

Ala Thr Ala Ser Ala Glu Gly Tyr Thr Pro Gly Glu Pro Trp Ser Thr
 20 25 30
 Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
 35 40 45
 Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
 50 55 60
 Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
 65 70 75 80
 Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala
 85 90 95
 Thr Pro Thr Ser Ser Glu Lys Ile
 100

<210> 6
 <211> 642
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> gene
 <222> (1)..(642)
 <223> TFP3

<400> 6
 gatcccgcc agcccttcca gcttttcttt ttccctttt gctacggtcg agacacggtc 60
 gcccaaaaga aacgggtcag cgtgtactgc gccaaaaaaa ttgcgcgcga titaagctaa 120
 acgtccacaa acaaaaacaa aaataagaaa taggttgaca gtgggtgaaa aattctcgaa 180
 ggtttcatct ccaaacagtc agtatataag taitcgggaa agagagccaa tctatcttgt 240
 ggtgggtcta tcttaacctt ctctttttgg cagtagtaat tgtaaatcaa gacacataaa 300
 actatttcac tcgctaaact tacatctaaa atgcaattca aaaacgtcgc cctagctgcc 360
 tcggttgctg ctctatccgc cactgcttct gctgaagggt aactccagg tgaacctagg 420
 tccaccttaa cccaaccgg ctccatctct tgtggtgctg ccgaatacac taccaccttt 480
 ggtattgctg ttcaagctat tacctcttca aaagctaaga gagacgttat ctctcaaatt 540
 ggtgacggtc aagtccaagc cactctgtct gctactgctc aagccaccga tagtcaagcc 600
 caagctacta ctaccgttac cccaaccagc tccgaaaaga tc 642

<210> 7
 <211> 50
 <212> PRT
 <213> *Hansenula polymorpha*

<220>
 <221> PEPTIDE
 <222> (1)..(50)
 <223> TFP4

<400> 7
 Met Arg Phe Ala Glu Phe Leu Val Val Phe Ala Thr Leu Gly Gly Gly
 1 5 10 15
 Met Ala Ala Pro Val Glu Ser Leu Ala Gly Thr Gln Arg Tyr Leu Val
 20 25 30
 Gln Met Lys Glu Arg Phe Thr Thr Glu Lys Leu Cys Ala Leu Asp Asp
 35 40 45
 Lys Ile
 50

<210> 8
 <211> 179
 <212> DNA
 <213> *Hansenula polymorpha*

<220>
 <221> gene
 <222> (1)..(179)
 <223> TFP4

<400> 8
 gatccgcttt ttattgcttt gctttgctaa tgagatttgc agaattcttg gtggtatttg 60
 ccacgttagg cggggggatg gctgcaccgg ttgagtctct ggccgggacc caacggatc 120
 tgggtgcaaat gaaggagcgg ttcaccacag agaagctgtg tgctttggac gacaagatc 179

<210> 9
 <211> 71
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <221> PEPTIDE
 <222> (1)..(71)
 <223> TFP1-3

<400> 9
 Met Phe Asn Arg Phe Asn Lys Phe Gln Ala Ala Val Ala Leu Ala Leu
 1 5 10 15
 Leu Ser Arg Gly Ala Leu Gly Asp Ser Tyr Thr Asn Ser Thr Ser Ser
 20 25 30
 Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala
 35 40 45
 Thr Ala Ser Asp Ser Leu Ser Ser Ser Asp Gly Thr Val Tyr Leu Pro
 50 55 60
 Ser Thr Thr Ile Ser Gly Asp
 65 70

<210> 10
 <211> 329
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> gene
 <222> (1)..(329)
 <223> TFP1-4

<400> 10
 ggatccatgt tcaatcgitt taacaaattc caagctgctg tcgctttggc cctactctct 60
 cgcggcgctc tcggtgactc ttacaccaat agcacctcct ccgcagactt gatttctatc 120
 acttcgctct cgtcagctag tgcaagtgcc accgcttccg actcactttc ttccagtgac 180
 ggtaccgitt atttgccatc cacaacaatt agcggtgatc tcacagttac tggtaaagta 240
 attgcaaccg aggcggtgga agtcgctgcc ggtggtaagt tgactttact tgacggtgaa 300
 aaatacgtct tctcatctga tctctatga 329

<210> 11
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
<223> JH97(Sfi-HSA-forward primer)

<400> 11
ccggccatta cgccgtgat gcacacaaga gtgag 35

<210> 12
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> JH119(Sfi-HSA-reverse primer)

<400> 12
ccggccgagg cggcctaagc ctaaggcag 29

<210> 13
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> JH99(Sfi-INV-forward primer)

<400> 13
gggcgccgc ctcggcccta gataaaaggt caatgacaaa cgaaactagc 50

<210> 14
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> JH100(Sall-INV-reverse primer)

<400> 14
ccgtcgactt actatatttac ttoccttact tg 32

<210> 15
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> JH106(Sfi-IL2-forward primer)

<400> 15
gcggccatta cgccgtgca cctacttcaa gttctac 37

<210> 16
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> JH107(Sfi-IL2-reverse primer)

<400> 16
gcggccatta cgccgtgca cctacttcaa gttctac 37

<210> 17
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
 <223> JH120(BamHI-IL2-1-forward primer)

<400> 17
 cgggatccgc acctacttca agttct 26

<210> 18
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> JH121(BamHI-IL2-2-forward primer)

<400> 18
 cgggatcctg cacctacttc aagttct 27

<210> 19
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> JH122(BamHI-IL2-3-forward primer)

<400> 19
 cgggatcctt gcacctactt caagttct 28

<210> 20
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> JH123(INV-1-reverse primer)

<400> 20
 ccatgaagg aaccaacaaa at 22

<210> 21
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> JH124(INV-forward primer)

<400> 21
 attttgttgg ttccttcaat gg 22

<210> 22
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> JH95(INV-2-reverse primer)

<400> 22
 ggctcgagct attttacttc ccttacttg 29

<210> 23
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
<223> JH132(SacI-GAL-forward primer)

<400> 23
gggagctcat cgcttcgctg att 23

<210> 24
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> JH137(IL-2-Term-reverse primer)

<400> 24
ccgtcgactt aagttagtgt tgagatg 27

<210> 25
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> HY22(TFP1-LDKR-reverse primer)

<400> 25
gaacttgaag taggtgccct tttatctaga ggatcagatg agaagac 47

<210> 26
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> HY23(TFP1-LDKR-forward primer)

<400> 26
tcttctcatc tgatcctcta gataaaaggg cacctacttc aagttc 46

<210> 27
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> HY20(TFP2-LDKR-reverse primer)

<400> 27
gaacttgaag taggtgccct tttatctaga ggatcgttca aactcc 46

<210> 28
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> HY21(TFP2-LDKR-forward primer)

<400> 28
ggagtttgaa cgatcctcta gataaaaggg cacctacttc aagttc 46

<210> 29
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
 <223> HY24(TFP4-LDKR-reverse primer)

<400> 29
 gaacttgaag taggtgccct tttatcaagg atcttgtcgt ccaaagc 47

<210> 30
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HY25(TFP4-LDKR-forward primer)

<400> 30
 gctttggacg acaagatcct tgataaaagg gcacctactt caagttc 47

<210> 31
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> JH143(XbaI-TFP1-d-reverse primer)

<400> 31
 cctctagaat caccgctaatt tgtttgtg 27

<210> 32
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> JH142(XbaI-TFP1-c-reverse primer)

<400> 32
 cctctagagg tgctattggt gtaagag 27

<210> 33
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> JH141(XbaI-TFP1-b-reverse primer)

<400> 33
 cctctagaac cgagagcgcc gcgagag 27

<210> 34
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> JH140(SpeI-XbaI-LDKR-forward primer)

<400> 34
 ggactagtct agataaaagg gcacc 25

<210> 35
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HY38(TFP1-UTR-forward primer)

<400> 35
 gaatttttga aaattcaagg atccatgttc aatcgtttta ac 42

<210> 36
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> JH144(GCSF-forward primer)

<400> 36
 cctctagata aaaggacccc cctgggccct gcc 33

<210> 37
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> JH145(GCSF-reverse primer)

<400> 37
 ggcagctgga tgtattttac atggggag 28

<210> 38
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HY17(TFP3-LDKR-reverse primer)

<400> 38
 gaacttgaag taggtgccct tttatcaagg atcttttcgg agc 43

<210> 39
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HY18(TFP3-LDKR-forward primer)

<400> 39
 gctccgaaaa gatccttgat aaaagggcac ctacttcaag ttc 43

<210> 40
 <211> 134
 <212> PRT
 <213> Saccharomyces cerevisiae

<220>
 <221> PEPTIDE
 <222> (1)..(134)
 <223> TFP3-1-1

<400> 40
 Met Gln Phe Lys Asn Val Ala Leu Ala Ala Ser Val Ala Ala Leu Ser
 1 5 10 15
 Ala Thr Ala Ser Ala Glu Gly Tyr Thr Pro Gly Glu Pro Trp Ser Thr
 20 25 30

PCTA9411-6.txt

Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
 35 40 45
 Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
 50 55 60
 Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
 65 70 75 80
 Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala
 85 90 95
 Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser
 100 105 110
 Thr Asn Ala Thr Ser Ser Ser Cys Ala Thr Pro Ser Leu Lys Asp Ser
 115 120 125
 Ser Cys Lys Asn Ser Gly
 130

<210> 41
 <211> 402
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> gene
 <222> (1)..(402)
 <223> TFP3-1-1

<400> 41
 atgcaattca aaaacgtcgc cctagctgcc tccgttgctg ctctatccgc cactgcttct 60
 gctgaagggtt aactccagg tgaaccatgg tccaccttaa ccccaaccgg ctccatctct 120
 tgtggtgctg ccgaatacac taccaccttt ggtattgctg ttcaagctat tacctcttca 180
 aaagctaaga gagacgttat ctctcaaatt ggtgacggtc aagtccaagc cacttctgct 240
 gctactgctc aagccaccga tagtcaagcc caagctacta ctaccgctac cccaaccagc 300
 tccgaaaaga tctcttcctc tgcatactaaa acatctacta atgccacatc atcttcttgt 360
 gccactccat ctttgaaaga tagctcatgt aagaattctg gt 402

<210> 42
 <211> 143
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <221> PEPTIDE
 <222> (1)..(143)
 <223> TFP3-1-2

<400> 42
 Met Gln Phe Lys Asn Val Ala Leu Ala Ala Ser Val Ala Ala Leu Ser
 1 5 10 15
 Ala Thr Ala Ser Ala Glu Gly Tyr Thr Pro Gly Glu Pro Trp Ser Thr
 20 25 30
 Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
 35 40 45
 Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
 50 55 60
 Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
 65 70 75 80
 Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala

PCTA9411-6.txt

85 90 95
 Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser
 100 105 110
 Thr Asn Ala Thr Ser Ser Ser Cys Ala Thr Pro Ser Leu Lys Asp Ser
 115 120 125
 Ser Cys Lys Asn Ser Gly Thr Leu Glu Leu Thr Leu Lys Asp Gly
 130 135 140

<210> 43
 <211> 429
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> gene
 <222> (1)..(429)
 <223> TFP3-1-2

<400> 43
 atgcaattca aaaacgtcgc cctagctgcc tccgttgctg ctctatccgc cactgcttct 60
 gctgaagggtt acactccagg tgaacatgg tccaccttaa cccaaccgg ctccatctct 120
 tgtggtgctg ccgaatacac taccaccttt ggtattgctg ttcaagctat tacctcttca 180
 aaagctaaga gagacgttat ctctcaaatt ggtgacggtc aagccaagc cacttctgct 240
 gctactgctc aagccaccga tagtcaagcc caagctacta ctaccgctac cccaaccagc 300
 tccgaaaaga tctcttcctc tgcactctaa acatctacta atgccacatc atcttcttgt 360
 gccactccat ctttgaagaa tagtcatgtt aagaattctg gtaccttaga attgaccttg 420
 aaggacggt 429

<210> 44
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BglII-GAP-forward primer

<400> 44
 gcaagatctg gatccttttt tgtag 25

<210> 45
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GAP-EcoRI-reverse primer

<400> 45
 aagaattctt gatagttggt caattg 26